**Amendments to the Drawings:**

The attached sheets of drawings include changes to Figs. 1-6. These sheets, which include Figs. 1-6 replace the original sheets

Attachment: Replacement Sheets

## REMARKS/ARGUMENTS

***Status of the claims***

Claims 14, 15 and new claims 21-29 are pending in the present application. Claims 22, 23, 28 and 29 explicitly refer to SEQ ID NO: 10, which is the polypeptide sequence encoded by SEQ ID NO: 9. Support for "90% sequence identity" recited in claims 21, 22, 26 and 28 is found, for example, in paragraph 30 of the present application. Claims 24-29 are directed to recombinant DNA vectors comprising the polynucleotides of the invention. Description of DNA vectors of the invention and their components is found, for example, in paragraphs 49-54 of the present application. No new matter is added by this amendment.

***Drawings***

The Drawings were objected to for being informal. Enclosed with this response are replacement sheets with corrected, formal drawings.

***Specification***

The specification was objected to for including sequences without sequence identifiers on page 14 of the specification. Applicants note that page 14 of the specification, in particular paragraph 64, has been previously amended to include sequence identifiers in the preliminary amendment filed September 12, 2005. If for some reason, this amendment is missing from the USPTO file, applicants would be happy to provide a copy.

***Rejections under 35 U.S.C. § 112, second paragraph***

Claim 14 stands rejected for allegedly being indefinite on a number of grounds. To expedite prosecution, this claim has been amended as suggested by the Examiner. In particular, the Examiner asserts that use of the term "comprising ... fewer than 522 amino acids" is unclear. Claim 14 has been amended to recite that the polypeptide "consists of ...fewer than 530 amino acids." Support for reference to 530 amino acids is found throughout the specification, for example, in claim 1, as filed. Reference to "80% identical" has been amended as suggested by the Examiner. Finally, increased salt tolerance is now explicitly recited to be compared to a plant that lacks the polynucleotide sequence of the invention. Support for this

amendment is replete throughout the specification, including claim 1, as filed. Each of the above amendments is made to expedite prosecution and do not narrow the scope of the claims, as filed. In view of the above, applicants respectfully request withdrawal of the rejections.

***Rejections under 35 U.S.C. § 112, first paragraph***

Enablement

The claims stand rejected for lacking enablement because it would allegedly require undue experimentation to make and use DNA molecules encoding polypeptides having 80% sequence identity to SEQ ID NO: 2, other than SEQ ID NO: 9. To support the rejection, the Examiner relies on Table 1 of the present application, which provides salt tolerance data for a large number of point mutations and truncated forms of SEQ ID NO: 2. Since the degree of salt tolerance varies among the different mutants, the Examiner asserts that one of skill could not predict which ones will work. While acknowledging that one of skill could readily make mutations in SEQ ID NO: 2, the Examiner further asserts that undue experimentation would be required to practice the claimed invention because there is allegedly no guidance as to regions within SEQ ID NO: 2 that can be modified.

It is well settled that the test of enablement is whether one reasonably skilled in the art could make or use the invention from the disclosures in the patent coupled with information known in the art without undue experimentation. The test is not whether ***any*** experimentation is necessary, but whether, if experimentation is necessary, it is undue.

Applicants respectfully disagree with the Examiner's position. As noted above, the Examiner acknowledges that SEQ ID NO: 9 is enabled and that making mutations in SEQ ID NO: 2 is routine. Thus, Applicants understand the Examiner's position to be that one of skill (1) lacks sufficient guidance as to which regions of SEQ ID NO: 2 (the AtNHX1 protein)can be modified and (2) would not know how to test such modified sequences, once they were made.

The information provided by Figure 6 of the present application is particularly relevant to the question of whether the specification provides sufficient guidance with regard to functional regions or domains in the AtNHX1 protein. Figure 6 illustrates the location of transmembrane domains, various binding domains (*e.g.,* the Na+ and H+ binding domains) and

the free N-terminal and C-terminal regions. Indeed, Figure 6 provides information about which amino acid residues make up each of these regions. Moreover, it shows the precise location of the 23 mutations (identified by the circled numbers) as well as sites of deletion for the six truncated forms referred to in Table 1 of the specification. Using the information provided in Table 6 in combination with Table 1, one of skill has extensive information about the structure and function of the AtNHX1 protein. Such information can be used to identify functional effect of entire regions of the protein. For example, as explained in Example 8 on page 18 of the specification, a truncated protein in which the free N-terminal sequence was deleted (NDL-1 in Table 1) provided enhanced salt tolerance. Based on this result, the inventors concluded that that the N-terminus is a negative regulator of function (*see* page 18, lines 8-10).

In light of the extensive teaching regarding structure of the protein in Table 6, including location of each amino acid in the protein, and the functional information for 29 mutant forms provided in Table 1, applicants believe a rejection based on an alleged lack of guidance in the present application simply cannot be maintained.

With regard to the ability to test mutant proteins for enhanced salt tolerance, the specification provides more than sufficient guidance. The Examiner must acknowledge this point in relying on Table 1 to support the rejection. There it can be seen that the present inventors were able to make and test 29 mutant proteins. The Examiner has presented no evidence to suggest that the yeast assays described in the specification are not entirely routine. As noted above, the test of enablement is not whether any experimentation is necessary, but whether, if experimentation is necessary, it is undue. In the absence of evidence that the assays used by the present inventors could not be routinely used by those of skill in the art, the Examiner's position cannot be maintained.

In light of the above, applicants respectfully submit that the Examiner has not established with sufficient reasoning or evidence that the present application lacks sufficient guidance to allow one of skill to make and use a wide variety of mutant sequences within the scope of the pending claims. In the absence of such a showing the rejection is improper and should be withdrawn.

Written Description

The Examiner has rejected claim 14 as allegedly failing to comply with the written description requirement. The rejection is based on an assertion that there are insufficient relevant identifying characteristics of variant protein sequences for one of skill to conclude that the inventors were in possession of the claimed invention.

Applicants respectfully disagree with the Examiner's position. Applicants maintain that the Examiner's apparent absolute requirement for actual reduction to practice of exemplary sequences in order demonstrate possession of the claimed invention is in conflict with the statutory requirements as well as the USPTO's own written description guidelines.

It is well accepted that a specification may, within the meaning of 35 U.S.C. 112, first paragraph, contain a written description of a broadly claimed invention ***without*** reducing to practice each and every species encompassed by the claims. In fact, the law does not even require that the specification describe the exact details for ***preparing every species*** within a claimed genus, much less the actual construction of the species themselves. Moreover, even if the Examiner considers the subject matter of the claims to be broader than that disclosed in the original specification, the written description requirement may be satisfied if the broader concept would naturally occur to one skilled in the art upon reading the earlier specification.

It is further well settled that possession of a genus may be satisfied through sufficient description of a "representative number of species" by: (a) an actual reduction to practice, (b) a reduction to drawings, or (c) disclosure of relevant, identifying characteristics, *i.e.*, structure or other physical and/or chemical properties, by functional characteristics coupled with known or disclosed correlation between function and structure, or by a combination of such identifying characteristics sufficient to show the applicant was in possession of the claimed genus. In other words, possession of a genus can be evidenced by describing the distinguishing identifying characteristics common to the divergent species encompassed. *See*, M.P.E.P. § 2163.02.

In this context, a "representative number of species" means that the species which are actually described are representative of the entire genus. Satisfactory disclosure of a representative number of species depends on whether one of skill in the art would recognize that

the applicant was in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed.

In this case, the claims encompass sequence variants of SEQ ID NO: 2. For example, claim 14 is directed to proteins with 80% sequence to SEQ ID NO: 2, while claims 21, 22, 26 and 28 are directed to proteins having 90% sequence identity to SEQ ID NO: 10. As noted above, the specification provides detailed sequence information about the AtNHX1 protein and a large number of mutants. As also explained above, the specification sets forth assays for preparing and identifying such variants. Accordingly, Applicants submit that the instant specification provides an adequate written description of the genus of sequence variants encompassed by the claims so as to convey with reasonable clarity to those skilled in the art that, as of the filing date sought, Applicants were in possession of the invention now claimed.

The facts of the present case are similar to those at issue in *Ex parte* Bandman (BPAI Appeal No. 2004-2319) ("Bandman") and *Ex parte* Sun (BPAI Appeal No. 2003-1993) ("Sun"). In Bandman, claims directed to an isolated polynucleotide encoding a polypeptide comprising an amino acid sequence at least 95% identical to a recited SEQ ID NO were rejected by an Examiner as failing to comply with the written description and enablement requirements. The Examiner alleged that the specification only provided a single species, and did not provide any disclosure of any particular structure to function/activity relationship in the single disclosed species. *See*, page 3 of the Bandman Decision. The specification in Bandman disclosed the complete structure of the polypeptide of the recited SEQ ID NO and a polynucleotide encoding it. The claims at issue in Bandman did not recite a function of the encoded protein. *See*, page 1 of the Bandman Decision.

In Sun, claims directed to an isolated polynucleotide at least 80% identical to a recited SEQ ID NO were rejected by an Examiner as failing to comply with the written description and enablement requirements. The Examiner alleged that the specification did not set forth what specific structural or physical features define the claimed isolated nucleic acids. The Examiner alleged that the skilled person could not predict the structure and function of isolated nucleic acid having at least 80% sequence identity to the recited SEQ ID NO. *See*, page 7 of the Sun Decision. The specification in Sun disclosed the complete structure of the

polynucleotide of the recited SEQ ID NO, and the encoded polypeptide. The claims at issue in Sun also did not recite a function of the encoded protein. *See*, pages 1-2 of the Sun Decision.

The BPAI reversed the Examiner's rejections under 35 U.S.C. § 112, first paragraph, in both Bandman and Sun, in each case stating that the specification described the complete sequence of the recited sequence and the genus limited to polypeptides or polynucleotides comprising 95% or 80% sequence identity to the recited SEQ ID NO. The BPAI noted that the Examiner had not adequately explained and/or provided evidence to support the assertion that the specification did not provide any disclosure of any particular structure to function/activity relationship in the single disclosed species. *See*, page 4 of the Bandman Decision and pages 7-10 of the Sun Decision.

Here, the claims are directed to a purified polynucleotide encoding a polypeptide that structurally shares at least about 80% amino acid sequence identity with SEQ ID NO: 2. and has the function of enhancing salt tolerance. Like the specifications at issue in Bandman and Sun, the present specification provides the full amino acid sequence of an exemplary protein. In addition, the specification provides detailed information regarding functional domains in the protein and provides sequence information for 29 sequence variants. In light of the above, the Examiner assertion that the specification does not provide disclosure of relevant identifying characteristics of the claimed sequences simply cannot be maintainer.

In summary, given the detailed disclosure of both the structure and function of the claimed polynucleotides, Applicants respectfully submit that a one of skill would find that the present specification provides a representative number of species sufficient to demonstrate possession of the claimed invention. Accordingly, withdrawal of the outstanding written description rejection is respectfully requested.

***Rejection under 35 U.S.C. § 102(b)***

Claims 14 and 15 stand rejected for allegedly being anticipated by Glaxiola *et al. Proc Nat Acad Sci* 96:1480-1485 (1999). Glaxiola *et al.* is cited to teaching the full length sequence of the AtNHX1 protein. The rejection is based on the Examiner assertion that the claims read on the full length protein because of the use of the term "comprising" in claim 14.

As noted above, the claim has been amended to clarify that only truncated forms of the protein are encompassed by the pending claims. In light of the above, applicants believe the rejection is improper and should be withdrawn.

## CONCLUSION

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested. If a telephone conference would expedite prosecution of this application, the Examiner is invited to telephone the undersigned at 415-576-0200.

Respectfully submitted,

/Kevin Bastian/

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